

Sequence alignment of various TGF β R isoforms (82210021, 82210017, AK102480, 8730021, 8730016, 40420011, 40420009, 30680882, 2phk_PhK, lir3_IRK, 1ias_TGFbR) across 1600 amino acids. The alignment highlights conserved regions and variable domains. Amino acids are color-coded by residue type: hydrophobic (black), polar (green), charged (red), and aromatic (blue).

Key features include:

- Conserved Regions:** Conserved blocks of amino acids are visible across all isoforms, particularly in the N-terminal and C-terminal regions.
- Variable Domains:** The alignment shows significant variation between isoforms, particularly in the extracellular domain (residues 100-500) and the intracellular kinase domain (residues 1400-1600).
- Color Coding:** Amino acids are color-coded based on their chemical properties: hydrophobic (black), polar (green), charged (red), and aromatic (blue).